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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,337

DATE: 01/25/2002
TIME: 11:56:57

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\01252002\I582337.raw

3 <110> APPLICANT: Japan Tobacco, Inc.
5 <120> TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
6 and Medicinal Uses Thereof
8 <130> FILE REFERENCE: J1-009PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/582,337
C--> 11 <141> CURRENT FILING DATE: 2000-06-23
13 <150> PRIOR APPLICATION NUMBER: JP P1997-367699
14 <151> PRIOR FILING DATE: 1997-12-25
16 <150> PRIOR APPLICATION NUMBER: JP P1998-356183
17 <151> PRIOR FILING DATE: 1998-12-15
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2338
25 <212> TYPE: DNA
26 <213> ORGANISM: Rat
28 <220> FEATURE:
29 <221> NAME/KEY: 5'UTR
30 <222> LOCATION: (1)..(212)
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (213)..(1256)
36 <220> FEATURE:
37 <221> NAME/KEY: 3'UTR
38 <222> LOCATION: (1257)..(2338)
40 <220> FEATURE:
41 <221> NAME/KEY: polyA_signal
42 <222> LOCATION: (2297)..(2302)
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47 gacggcagca gccccagccc agtggacaac cccaggagcc accacacctgga gcgtccggac 120
49 accaacacctcc gccccgagac cgagtcagg ctccggccgc gcccctcgctc gcctctgcac 180
51 cccgctgtgc gtcctctgtgc cgcgccccga cc atg ctc gcc tcc gtc gcg ggt 233
52 Met Leu Ala Ser Val Ala Gly
53 1 5
55 ccc gtt agc ctc gcc ttg gtg ctc ctc tgc acc cgg cct gcc acc 281
56 Pro Val Ser Leu Ala Leu Val Leu Leu Cys Thr Arg Pro Ala Thr
57 10 15 20
59 ggc cag gac tgc agc gcg cag tgt cag tgc gca cgt gaa gcg gcg ccg 329
60 Gly Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Arg Glu Ala Ala Pro
61 25 30 35
63 cgc tgc ccc gcc ggc gtg agc ctg gtg gac ggc tgc ggc tgc tgc 377
64 Arg Cys Pro Ala Gly Val Ser Leu Val Asp Gly Cys Gly Cys Cys

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65	40	45	50	55	
67	cgc gtc tgc gcc aag cag ctg gga gaa ctg tgc acg gag cgt gat ccc				425
68	Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro				
69	60	65	70		
71	tgc gac cca cac aag ggt ctc ttc tgc gac ttc ggc tcc ccc gcc aac				473
72	Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn				
73	75	80	85		
75	cgc aag att ggc gtg tgc cct gcc aaa gat ggt gca ccc tgt gtc ttc				521
76	Arg Lys Ile Gly Val Cys Pro Ala Lys Asp Gly Ala Pro Cys Val Phe				
77	90	95	100		
79	ggt ggg tcc gtg tac cgc agc ggc gag tcc ttc caa agc agt tgc aaa				569
80	Gly Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys				
81	105	110	115		
83	tac cag tgc act tgc ctg gat ggg gcc gtg ggc tgt gtg ccc ctg tgc				617
84	Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys				
85	120	125	130	135	
87	agc atg gac gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg				665
88	Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg				
89	140	145	150		
91	gtc aag ctg ccc ggg aaa tgc tgt gag gag tgg gtg tgt gat gag ccc				713
92	Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro				
93	155	160	165		
95	aag gac cgc aca gtg gtt ggc cct gcc cta gct gcc tac cga ctg gaa				761
96	Lys Asp Arg Thr Val Val Gly Pro Ala Leu Ala Tyr Arg Leu Glu				
97	170	175	180		
99	gac aca ttt ggc cct gac cca act atg atg cga gcc aac tgc ctg gtc				809
100	Asp Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val				
101	185	190	195		
103	cag acc aca gag tgg agc gcc tgt tct aag acc tgt ggg atg ggc atc				857
104	Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile				
105	200	205	210	215	
107	tcc acc cgg gtt acc aat gac aat acc ttc tgc agg ctg gag aag cag				905
108	Ser Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln				
109	220	225	230		
111	agt cgt ctc tgc atg gtc agg ccc tgt gaa gct gac cta gag gaa aac				953
112	Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn				
113	235	240	245		
115	att aag aag ggc aaa aag tgc atc cgg acg cct aaa att gcc aag cct				1001
116	Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro				
117	250	255	260		
119	gtc aag ttt gag ctt tct ggc tgc acc agt gtg aag acc tac cgg gct				1049
120	Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala				
121	265	270	275		
123	aag ttc tgt ggg gtg tgc acg gac ggc cgc tgc tgc aca ccg cac aga				1097
124	Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg				
125	280	285	290	295	
127	acc acc aca ctg ccg gtg gag ttc aag tgc ccc gat ggc gag atc atg				
128	Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met				
129	300	305	310		

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131 aaa aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1193
 132 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys
 133 315 320 325
 135 ccc ggg gac aat gac atc ttt gag tcc ttg tac tac agg aag atg tat 1241
 136 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr
 137 330 335 340
 139 gga gac atg gcg taa agccagggag taagggacac gaactcattt agactataac 1296
 140 Gly Asp Met Ala
 141 345
 143 ttgaactgag ttacatctca ttttcttctg taaaaaaaaac aaaaagggtt acagtagcac 1356
 145 attaatttaa atctgggttc ctaactgctg tggagaaaa caccacccacccg aagtgagaac 1416
 147 cgtgtgtcat tgtcatgcaa atagcctgtc aatctcagac actgggttcg agacagttt 1476
 149 gacttgcacag ttgttcaacta ggcacatgtt acagaacgc cactaagggtg agcctcctgg 1536
 151 aagagtggag atgccaggag aaagacaggt actagctgag gtcattttaa aagcagcgtat 1596
 153 atgcctactt tttggagtgtt gacagggag ggacattata gcttgcttcg agacagaccc 1656
 155 gctctagcaa gagctgggtg tttgttcctcc actcggttag gctgaagcca gctattctt 1716
 157 cagtaagaac agcagtttca ggcgtgacat tctgatttca gggacactgg tcgggagtca 1776
 159 gaaccttgc tattagactg gacagctgtt ggcaagtgaa ttggccgtt acaagccaga 1836
 161 ttttatgga tcttgtaaat attgtggata aatataatata tttgtacagt tatctargtt 1896
 163 aatttaaaga cgtttgc tattgttctt gtttaagtg cttttggaaat ttttaactg 1956
 165 atagcctcaa actccaaaca ccatcgatag gacataaaagc ttgtctgtca ttcaaaacaa 2016
 167 aggagatact gcagtgaaaa ctgtaacctg agtactgtc tgtcagaaca tatggtagt 2076
 169 agacggtaaa gcaatggatc agaagtcaaa tttcttagtag gaaatgtaaa atactgtt 2136
 171 gccaacaaat ggcctttatt aagaaatggc ttgctcaggg taactggtca gatttccacg 2196
 173 aggaagtgtt tgctgcttct ttgactatga ctggggggg aggcaatgtt tttgttggaa 2256
 175 gtgtgaccaa aagttacatg tttgcaccc tctagttgaa aataaaagtat atatatttt 2316
 177 tatatgaaaa aaaaaaaaaaa aa 2338
 180 <210> SEQ ID NO: 2
 181 <211> LENGTH: 347
 182 <212> TYPE: PRT
 183 <213> ORGANISM: Rat
 185 <400> SEQUENCE: 2
 186 Met Leu Ala Ser Val Ala Gly Pro Val Ser Leu Ala Leu Val Leu Leu
 187 1 5 10 15
 189 Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys Gln
 190 20 25 30
 192 Cys Ala Arg Glu Ala Ala Pro Arg Cys Pro Ala Gly Val Ser Leu Val
 193 35 40 45
 195 Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly Glu
 196 50 55 60
 198 Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe Cys
 199 65 70 75 80
 201 Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Pro Ala Lys
 202 85 90 95
 204 Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly Glu
 205 100 105 110
 207 Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly Ala
 208 115 120 125
 210 Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser Pro

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211 130 135 140
213 Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu
214 145 150 155 160
216 Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Val Val Gly Pro Ala
217 165 170 175
219 Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr Met
220 180 185 190
222 Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys Ser
223 195 200 205
225 Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Thr
226 210 215 220
228 Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro Cys
229 225 230 235 240
231 Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg
232 245 250 255
234 Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys Thr
235 260 265 270
237 Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp Gly
238 275 280 285
240 Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe Lys
241 290 295 300
243 Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys Thr
244 305 310 315 320
246 Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu Ser
247 325 330 335
249 Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
250 340 345
253 <210> SEQ ID NO: 3
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
260 synthesized primer sequence
262 <220> FEATURE:
263 <221> NAME/KEY: primer_bind
264 <222> LOCATION: (1)..(20)
266 <400> SEQUENCE: 3
267 tgcggctgct gccgctgtctg 20
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 21
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
277 synthesized primer sequence
279 <220> FEATURE:
280 <221> NAME/KEY: primer_bind
281 <222> LOCATION: (1)..(21)

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283 <400> SEQUENCE: 4
284 gcacaggctc tgatgaacat c 21
287 <210> SEQ ID NO: 5
288 <211> LENGTH: 444
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(444)
296 <220> FEATURE:
297 <221> NAME/KEY: sig_peptide
298 <222> LOCATION: (1)..(57)
300 <220> FEATURE:
301 <221> NAME/KEY: V_region
302 <222> LOCATION: (58)..(363)
304 <400> SEQUENCE: 5
305 atg gag ttt ggg ctg agc tgg att ttc ctt gct gct att tta aaa ggt 48
306 Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
307 1 5 10 15
309 gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag 96
310 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys
311 20 25 30
313 cct ggg ggg tcc ctt aag acc tct cct gtg cag cct ctg gat tca act 144
314 Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr
315 35 40 45
317 ttc agt aac gcc tgg atg agc tgg gtc cgc cag gct cca gga agg ggc 192
318 Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly
319 50 55 60
321 tgg agt ggg ttg gcc gta tta aaa gca aaa ctg atg gtg gga cac aca 240
322 Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr
323 65 70 75 80
325 gac tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat 288
326 Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp
327 85 90 95
329 tca aaa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gag gac 336
330 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
331 100 105 110
333 aca gcc gtg tat tac tgt acc aca aaa tgg gtg gct acg gac tac ttt 384
334 Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe
335 115 120 125
337 gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc 432
338 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
339 130 135 140
341 aag ggc cca tcg 444
342 Lys Gly Pro Ser
343 145
346 <210> SEQ ID NO: 6
347 <211> LENGTH: 148
348 <212> TYPE: PRT

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/582,337

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TIME: 11:56:58

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\01252002\I582337.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date